

Tue Mar 4 15:58:08 2003

us-10-000-213-3.rge

Page 23

Q7 1016 ACCAAAGGAGACACACGCTGGAGCCTGCATCAACAAGTCC 1064
||||| - || - || - || - || - || - ||
991 ACCAAAGGATGCTACGRRRACCTCGGGAGTCCTTTTTCAGCTCC 949

Source compiled: March 2, 2003, 17:46:05
Job time: 12820 secs



diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

Claim 1; SEQ ID No 5109; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligonucleotides, and for chromosome mapping and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving loss of normal activity of (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on RNA and amino acid sequences. AAS64197 AAS34564 represent novel human diatomic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published.pct.sequences](http://wipo.int/pub/published.pct.sequences).

Sequence 4604 BP; 1114 A; 1278 C; 1197 G; 1015 T; 0 other;

```
.Query Match 100.0%; Score 4604; DB 23; Length 4604;
Best Local Similarity 100.0%; Prod No 6;
Matches 4604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]


```

DB 3841 CTGGCTTGTAACTTCAATCAAGGCTATATAGAAAGAGAAAGAGAGATCAATCTGCGCTC 3900
QY 3901 AATGGAATCAGACATCTATCTCAATCAATGATGATGATGATGATGATGATGATGATGATGAT 3960
DB 3901 AATGGAATCAGACATCTATCTCAATCAATGATGATGATGATGATGATGATGATGATGATGAT 3960
QY 3961 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4020
DB 3961 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4020
QY 4021 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4080
DB 4021 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4080
QY 4081 CCTGGGCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 4140
DB 4081 CCTGGGCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 4140
QY 4141 AAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4200
DB 4141 AAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4200
QY 4201 TACTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4260
DB 4201 TACTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4260
QY 4261 TTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4320
DB 4261 TTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4320
QY 4321 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4380
DB 4321 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4380
QY 4381 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4440
DB 4381 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4440
QY 4441 AACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4500
DB 4441 AACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4500
QY 4501 AACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4560
DB 4501 AACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4560
QY 4561 CTTTCTTTCAGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4604
DB 4561 CTTTCTTTCAGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4604

```

RESULTS 2

AAV41427

ID AAV41327 strand 1, DNA, 4701 bp.

XX AC AAV41327;

XX AC AAV41327;

XX AC AAV41327;

XX AC AAV41327;

XX AC AAV41327;

XX AC AAV41327;

XX AC AAV41327;

XX AC AAV41327;

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XX AC AAV41327;

XX AC AAV41327;

XX AC AAV41327;

XX AC AAV41327;

XX AC AAV41327;

XX AC AAV41327;


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1056 AGGTCATCAATTTGGTTCATTAAGTCTTCCACCAAGACACATGCTGCTGGATGCTG 1115
QY 981 GAAACCAAGACATCAACTACGGGCTGACATAGTGTGATTAAGATGATACATCTTGAC 1040
DB 1116 GAAACCAAGACATCAACTACGGGCTGACATAGTGTGATTAAGATGATACATCTTGAC 1175
QY 1041 TGATTAGAGCGCTTCATCAAGTCTGACATGATGATGATGATGATGATGATGATGAT 1100
DB 1176 TGATTAGAGCGCTTCATCAAGTCTGACATGATGATGATGATGATGATGATGATGAT 1235
QY 1101 AGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1160
DB 1236 AGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1295
QY 1161 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1220
DB 1296 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1355
QY 1221 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1280
DB 1356 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1415
QY 1281 ACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1340
DB 1416 ACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1475
QY 1341 AGTGCAGATCAAGCTAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1399
DB 1476 AGTGCAGATCAAGCTAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1534

RESULT 12
AAV03124
ID AAV04124 standard, cDNA, 1960 bp.
XX
AC AAV04124:
XX
DI 11-JUN-1998 (first entry)
XX
DE cDNA encoding rat vitamin D receptor (VDR0).
XX
KW Rat; vitamin D receptor; isoform proteol. VDR1; VDR0; diagnosis;
KW dominant negative receptor; signal transmission channel;
KW bone density disorder, screening, ds
XX
GS Rattus rattus.
XX
FH Key
FT CDS 12..1283
FT /tag= a
FT /transl_except= (pos:1080-1091, aa:Gly)
XX
PN W09747172-A1.
XX
PD 18-DEC-1997.
XX
PF 10-JUN-1997. 97M0-IR00947
XX
PR 10-JUN-1996. 96JP-0194179.
XX
PA (CHUS ) CHUGAI PHARM CO.LTD.
XX (CHUS ) CHUGAI SEIYAKU KK
XX
FI Kato, S. 56-60 K.
XX
UR WP1: 1998-051917/05.
XX P-PSDB; AAN47509.
XX
PT DNA encoding a vitamin D receptor isoform protein - useful for bone
PT density determination and for screening substances for vitamin D
PT activity
XX
PS Disclosure: Fig 1; 46pp; Japanese.

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XX A novel cDNA sequence encodes the rat vitamin D receptor isoform
XX protein (VDR1) the isoform differs from the normal receptor
XX (VDR0), which is encoded by the present sequence, in having the
XX vitamin D response element curtailed by 85 residues, and having an
XX extra 19 residues inserted at the C-terminal of this element. It
XX acts as a dominant negative receptor in the vitamin D signal
XX transmission channel.
XX the isoform protein can be used to diagnose bone density disorders,
XX and screen for substances having potential vitamin D-like activity.
XX
SQ Sequence 1960 bp: 432 A; 620 C; 497 G; 411 T; 0 other;
XX
Query Match 24.5%; Score 1129.6; DB 19; Length 1960;
Best local Similarity 81.5%; Ref. No. 4350 264;
Matches 140; Conservative 0; Mismatches 284; Indels 40; Gaps 9;
QY 105 CTCTTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 164
DB 1 CTCTTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
QY 165 ACCGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 224
DB 61 ACCGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 225 ATCTATATATATATATATATATATATATATATATATATATATATATATATATATAT 284
DB 121 ATCTATATATATATATATATATATATATATATATATATATATATATATATATATAT 180
QY 285 TATTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 344
DB 181 TATTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 345 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 404
DB 241 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 400
QY 405 ATGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 464
DB 301 ATGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 465 ATGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 524
DB 361 ATGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 525 ACCGCCACCAATGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
DB 421 ACCGCCACCAATGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 585 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 644
DB 481 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528
QY 645 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 704
DB 529 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
QY 705 TGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 764
DB 589 TGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 648
QY 765 TGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 824
DB 649 TGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
QY 825 GCAATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 884
DB 709 GCAATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
QY 885 AGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944
DB 769 AGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 828

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[illegible]

Search completed: March 2, 2003, 11:17:20
Job time : 1168 secs

TELEPHONE: 414-277-5715
 TELEFAX: 414-277-5774
 INFORMATION FOR SPQ ID NO: 6;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2048 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 Molecule TYPE: cDNA
 HYPOHETICAL: No
 ANTI SENSE: No
 ORIGINAL SOURCE:
 ORGANISM: Rat
 PUBLICATION INFORMATION:
 AUTHORS: Burmester, James K.,
 Wiese, Russel J.,
 Maeda, No. 5260199yo
 AUTHORS: Boland, heet F.
 TITLE: Structure and regulation of the rat
 1,25-dihydroxyvitamin D₃ receptor
 JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
 VOLUME: 85
 PAGES: 9499-9502
 DATE: December 1988
 US 07 737 746 B 6

Query Match 25.1%; Score 1154; Db 1; Length 2043;
 best local similarity 81.1%; Pred. No. 3 50-247;
 Matches 1441; Conservative 0; Mismatches 300; Indels 47; Gaps 11;

QY	21	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	80
DB	7	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	65
QY	81	GGGCTGCTACTTACCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	140
DB	66	GGGCTGCTACTTACCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	119
QY	141	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	200
DB	120	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	179
QY	201	AGGAGGCTGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	260
DB	180	AGGAGGCTGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	239
QY	261	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	320
DB	240	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	299
QY	321	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	380
DB	300	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	359
QY	381	GGGAGGCTGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	440
DB	360	GGGAGGCTGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	419
QY	441	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	500
DB	420	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	479
QY	501	AGGAGGCTGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	560
DB	480	AGGAGGCTGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	539
QY	561	AGGAGGCTGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	620
DB	540	AGGAGGCTGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	599
QY	621	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	680
DB	600	CGGCGGAAACAAAGGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	647

QY	681	ACGTGATACAGCTCTTCACAGACATGATGAGATCTGCTGAGAGTTCTCTCAATCTGATCTGATG	740
DB	648	TGTAACACCACTCTCAGTACAGATGATGAGATCTGCTGAGAGTTCTCTCAATCTGATCTGATG	707
QY	741	AGCAAGATTACAGTCACTCTGCTGAGAGTCTGCTGAGAGTTCTCTCAATCTGATCTGATG	800
DB	708	GAGAGGATTCTGATGAGAGTCTGCTGAGAGTCTGCTGAGAGTTCTCTCAATCTGATCTGATG	767
QY	801	ATCTGCTGAGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	860
DB	768	ACTCTGCTGAGCTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	827
QY	861	CAGGATTCAGAGACCTTCACTCTGAGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	920
DB	828	CAGGATTCAGAGACCTTCACTCTGAGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	887
QY	921	AGTCTATCATGTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	980
DB	888	AGTCTATCATGTTGGTGGTGAAGTGTCTGGAGAGTCTCACAGAGACAGACGCC	947
QY	981	CTAAGCTACAGTCACTCTGAGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1040
DB	948	CTAAGCTACAGTCACTCTGAGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1007
QY	1041	TGATTCAGTCTGCTCATTAAGTCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1100
DB	1008	TGATTCAGTCTGCTCATTAAGTCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1067
QY	1101	AGCATCTCTGCTCATTAAGTCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1160
DB	1068	AGCATCTCTGCTCATTAAGTCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1127
QY	1161	CGGCTGATTCAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1220
DB	1128	CGGCTGATTCAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1187
QY	1221	CGGCTGATTCAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1280
DB	1188	CGGCTGATTCAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1247
QY	1281	ACCTGCGGAGCTCTCAATGAGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1340
DB	1248	ACCTGCGGAGCTCTCAATGAGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1307
QY	1341	AGTGGAGCTGAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1400
DB	1308	AGTGGAGCTGAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1367
QY	1401	TAGAGAGCTGAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1457
DB	1368	TAGAGAGCTGAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1427
QY	1458	CGGCTGATTCAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1516
DB	1428	CGGCTGATTCAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1487
QY	1517	GCCAGCTGCTCTATGAGAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1574
DB	1488	GCCAGCTGCTCTATGAGAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1547
QY	1575	-----GCGGAGTCTTTCAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1622
DB	1548	CTTCTGCTGAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1607
QY	1624	TTTCTTTCAGAGAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1682
DB	1608	TTTCTTTCAGAGAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1667
QY	1683	C---AGAGATGCTCTGAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1740
DB	1668	CTAGAGATGCTCTGAGAGTCTGATCTGAGAGTCTGATCTGAGAGTCTCACAGAGACAGACGCC	1722

RESULT 11
US-GB-545-058A-5/c
; Sequence 5, Application US/95535058A
; Patent No. 5770420
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF GLYCOSAMINOGLYCAN STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #10, Version #1 25
; CURRENT APPLICATION DATA:
; ALL: A: N NMREF IL: G FSC 058A
; FILING DATE:





Genature version 5.1.4 j6.4578
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nm nucleide nucleic search, using sw model

Run on: March 2, 2003, 14:02:44 : Search time 5576 seconds

(without alignments)

13386,718 Million cell updates/sec

Title: US 10-000-213-3

Reflected score: 4604

Sequence: 1 gaaacagcttgctacacgcgc

Scoring table: 1DENITLY_N00

Gapop 10.0 : Gapov 1.0

Searched: 16154096 seqs, 8097743476 residues

Total number of hits satisfying chosen parameters: 32,602,332

Minimum lds seq length: 0

Maximum lds seq length: 2000000000

Post processing: Minimum Match 9%

Maximum Match 100%

Lasting first 45 summaries

Database: EST:*

1: em_est1a:*

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3: em_est1a:*

4: em_est1a:*

5: em_est1a:*

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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	809	17.6	847	9	AU140214	AU140214
2	804	17.4	997	14	BM462824	BM462824
3	786.6	17.1	1048	14	BQ054557	BQ054557
4	743.8	16.2	876	14	BQ281474	BQ281474
5	739.8	16.1	1037	14	BQ067521	BQ067521
6	659.8	14.3	1106	14	BM908433	BM908433

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C	7	649.8	14.1	725	14	BQ007624
B	8	642.8	14.0	708	10	BE330042
9	639.8	13.9	866	13	B1821706	
10	634.4	13.8	771	10	BE385638	
C	11	631.4	13.7	843	9	A1454054
12	618.4	13.4	665	10	BE390515	
C	13	610.2	13.3	822	9	AA772158
C	14	607.2	13.2	677	14	BQ052462
C	15	605.4	13.1	694	9	A1402811
C	16	595	12.9	1051	13	B1656698
C	17	591	12.8	665	9	A1874446
18	585.2	12.7	1031	14	BQ671215	
19	584.8	12.7	622	12	BG149660	
C	20	584.6	12.7	656	9	A1923720
C	21	579.8	12.6	687	9	A1989943
22	573	12.4	634	9	A1031652	
23	568.4	12.3	606	13	BM264426	
C	24	565.6	12.3	617	9	AA772285
C	25	565.4	12.3	684	9	AA556449
C	26	564.8	12.3	622	14	BQ002808
27	559	12.1	594	14	BM764797	
C	28	555.4	12.1	612	13	BM264731
C	29	553.6	12.0	687	10	AA057784
C	30	550.8	12.0	618	9	A1458267
31	550.8	12.0	625	13	B1824001	
32	546.8	11.9	584	9	AA855043	
33	544.6	11.8	584	9	AA706718	
34	544.6	11.8	618	9	A1055874	
C	35	544.6	11.8	682	9	AA646855
36	541.8	11.8	579	10	BE676532	
C	37	537.4	11.7	577	12	BQ661265
38	537	11.7	570	14	BM850555	
39	535	11.6	577	9	A1016571	
40	533.4	11.6	568	9	A1052108	
41	530	11.5	554	14	BM745741	
C	42	529.8	11.5	554	13	BM127733
43	529.8	11.5	562	9	A1949243	
44	529.8	11.5	562	10	AA874285	
45	529.4	11.5	554	9	AA724615	

ALIGNMENTS

RESULT 1	AU140214	847 bp	mRNA	linear	EST 05 AUG 2002
LOCUS	AU140214	PLACE2 Homo sapiens cDNA clone	FLAC2000147 5', mRNA		
DEFINITION	AU140214	sequence.			
ACCESSION	AU140214				
VERSION	AU140214.1	GI:11001745			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 847)				
AUTHORS	Ota, T., Suzuki, Y., Saito, K., Ishii, S., Yamamoto, J., Sugiyama, T., Nishikawa, T., Nakamura, Y., Sugano, S., Masuko, Y. and Iwata, T.				
TITLE	HLI human cDNA project (Ota, T., Suzuki, Y., Saito, K., Ishii, S., Yamamoto, J., Sugiyama, T., Nishikawa, T., Nakamura, Y., Sugano, S., Masuko, Y., Iwata, T.)				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Takao Iwata Genomics Laboratory Helix Research Institute 1542-3 Yama, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp URL: human cDNA project 5' & 3' end one-pass sequence list, Helix Research Institute cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and				

[illegible]


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QY 4424 GACAGCAGAAAGCATGTAACACAGTGTCTCTCTATCATTTTCAAAAGAGAAAAAGTTGGC 4483
Db 197 GTCAGCCGCAAGGATGTAACACAGTGTCTCTCTATCATTTTCAAAAGAGAAAAAGTTGGC 138
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Db 77 TACTTATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 19

RESULT 15
AI302811.1
LOCUS AI302811.1
DEFINITION qu549g7 xl N1-CCAP_Kid5 Homo sapiens cDNA (NM_015624.2)
ACCESSION AI302811
VERSION AI302811
KEYWORDS VITAMIN D3 RECEPTOR (HUMAN); mRNA sequence.
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 694)
AUTHORS NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap/
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Streusberg, Ph.D.
Email: eqabbs@mail.nih.gov
Tissue Procurement: Christopher Miskaik, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CCAP clone distribution information can be
found through the I M A G E Consortium/Link at:
www.bio.lni.gov/bbrp/image/image.html
Insert Length: 684 bp Error: 0.00
Seq primer: -400p from Gibco
High quality sequence stop: 464.
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/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/notes="organ: kidney; Vector: pTZ19-pac (Pharmacia) with
a modified polylinker; Site: 1. Not 1. Site: 2. Eco RI; 1st
strand cDNA was primed with a Not 1 oligo(dT) primer [5',
AATCGGAAGATTCGGCCGCAATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not 1 and cloned into the Not 1
and Eco RI sites of the modified pTZ19 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 176 a 162 c 136 g 219 t
ORIGIN
Query Match 13.1%; Score 605.4; DB 9; Length 694;
Best Local Similarity 96.28; Pred. No. 1.1e-83;
Matches 662; Conservative 0; Mismatches 22; Indels 4; Gaps 4;
QY 4919 CCCCACACATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3978
Db 693 CACCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
QY 4979 GGTGATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 4038

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Db 634 GATTCATCAIAAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 575
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QY 4097 CAGGAGCAGTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4156
Db 514 CAGGAGCAGTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 445
QY 4157 AGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4216
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